



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/676,873A

DATE: 08/23/2004
TIME: 11:15:35

Input Set : A:\COTH-P01-002.TXT
Output Set: N:\CRF4\08232004\J676873A.raw

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4 <110> APPLICANT: Chan, John
5     Baynes, Brian
6     Zhang, Shengsheng
8 <120> TITLE OF INVENTION: METHODS OF ENGINEERING SPATIALLY
9     CONSERVED MOTIFS IN POLYPEPTIDES
12 <130> FILE REFERENCE: COTH-P01-002
14 <140> CURRENT APPLICATION NUMBER: US 10/676,873A
15 <141> CURRENT FILING DATE: 2003-09-30
17 <150> PRIOR APPLICATION NUMBER: US 60/414,688
18 <151> PRIOR FILING DATE: 2002-09-30
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 474
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Nucleotide sequence of TNF alpha chain b mutation
31     b_tyro_119_asp
33 <400> SEQUENCE: 1
34 gtcagatcat cttctcgAAC cccgagtGAC aaggcTGTAG cccatgttGt agcaaaccct 60
35 caagctgagg ggcagctcca gtggctgaac cgccgggcca atgcctcct ggcctaattggc 120
36 gtggagctga gagataacca gctgggtggt ccattcagagg gcctgtacct catctactcc 180
37 caggcctct tcaaggggcca aggctggccc tccacccatg tgctcctcac ccacaccatc 240
38 agccgcatacg ccgtctcta ccagaccaag gtcaacccctcc tctctgccc caagagcccc 300
39 tgccagaggg agaccccaaga gggggctgag gccaaggccct ggtatgagcc catcgatctg 360
40 ggaggggtct tccagctgga gaagggtgac cgactcagcg ctgagatcaa tcggccgac 420
41 tatctcgact ttgccgagtc tggcaggtc tactttggta tcattgccct gtga        474
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44 <211> LENGTH: 157
45 <212> TYPE: PRT
46 <213> ORGANISM: Artificial Sequence
48 <220> FEATURE:
49 <223> OTHER INFORMATION: Protein sequence of TNF alpha chain b mutation
50     b_tyro_119_asp
52 <400> SEQUENCE: 2
53 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala Gly Val
54     1           5           10          15
55 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
56     20          25           30
57 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
58     35          40           45
59 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe

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60      50          55          60
61 Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
62 65          70          75          80
63 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
64          85          90          95
65 Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
66          100         105         110
67 Pro Gln Tyr Glu Pro Ile Asp Leu Gly Gly Val Phe Gln Leu Glu Lys
68          115         120         125
69 Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Leu Phe
70          130         135         140
71 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
72 145          150          155
75 <210> SEQ ID NO: 3
76 <211> LENGTH: 474
77 <212> TYPE: DNA
78 <213> ORGANISM: Artificial Sequence
80 <220> FEATURE:
81 <223> OTHER INFORMATION: Nucleotide sequence of TNF alpha chain c mutations
82     c_tyr_119_his, c_tyr_59_ser
84 <400> SEQUENCE: 3
85 gtcagatcat cttctcgAAC cccgagtGAC aaggcTGTAG cccatgttGT agcaaaccCT 60
86 caagctgagg ggcagctCCA gtggctGAAC cggcgggCca atgcCCTCCT ggccaatggc 120
87 gtggagctGA gagataacCA gctggTggT ccatcagagg gcctgtacCT catcagtTCC 180
88 caggTCCTCT tcaaggGCCA aggCTGCCCT tccacCCATG tgctcCTCac ccacaccATC 240
89 agccgcATCG ccgtCTCCTA ccagaccaAG gtcaacCTCC tCTCTGCCAT caagAGCCCC 300
90 tgccagagGG agacCCCAGA gggggCTGAG gccaaggCCCT ggtatgAGCC catccatCTG 360
91 ggaggGGTCT tccagCTGGA gaaggGTGAC cgactcAGCG ctgagatCAA tcggccccGAC 420
92 tatCTCGACT ttGCCGAGTC tggcCAGGTC tactTTGGGA tcattGCCCT gtGA        474
94 <210> SEQ ID NO: 4
95 <211> LENGTH: 157
96 <212> TYPE: PRT
97 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Protein sequence of TNF alpha chain c mutations
101     c_tyr_119_his, c_tyr_59_ser
103 <400> SEQUENCE: 4
104 Val Arg Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
105 1          5          10          15
106 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
107 20          25          30
108 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
109 35          40          45
110 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Ser Ser Gln Val Leu Phe
111 50          55          60
112 Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
113 65          70          75          80
114 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
115          85          90          95

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116 Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
117 100 105 110
118 Pro Gln Tyr Glu Pro Ile His Leu Gly Gly Val Phe Gln Leu Glu Lys
119 115 120 125
120 Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Leu Phe
121 130 135 140
122 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
123 145 150 155

VERIFICATION SUMMARY

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